

SEQUENCE LISTING

Underlining in each sequence indicates location of the chromophore domain.

Potential cysteine attachment sites are indicated in boldface.

Cph1: Locus SLR0473 = S6803PHY1 = SYN_PHY (Yeh *et al*, 277:1505-15-8 (1997)), a 748 aa protein.

SEQ ID NO:1

MATTVQLSDQSLRQLETLAIHTAHLIQPHGLVVVLQEPDLTISQISANCTGILGRSPED
LLGRTLGEVFDSEFQIDPIQSRLTAGQISSLNPSKLWARVMGDDFVIFDGVFHRNSDGL
LVCELEPAYTSDNLPFLGFYHMANAALNRLRQQANLRDFYDVIVEEVRRMTGFDR
VMLYRFDENNHGVDIAEDKRDDMEPYLGLHYPESDIPQPARRLFHNPPIRVIPDVYG
VAVPLTPAVNPSTNRAVDLTESILRSAYHCHLTYLKNMGVGASLTISLIKDGHLWGL
IACHHQTPKVIPFELRKACEFFGRVVFESNISAQEDTETFDYRVQLAEHEAVLLDKMT
TAADFVEGLTNHPDRLLGLTGSQGAACFGEKLILVGETPDEKAVQYLLQWLENRE
VQDVFFTSSLSQIYPDAVNFKSVASGLLAIPARHNFLWFRPEVLQTVNWGGDPNH
AYEATQEDGKIELHPRQSFDLWKEIVRLQSLPWQSVEIQSALALKKAIVNLILRQAE
LAQLARNLERSNADLKKFAYIASHDLQEPLNQVSNYVQLLEMRYSEALDEDAKDFI
DFAVTGVSLMQTLIDDILTYAKVDTQYAQLTFTDVQEVVDKALANLKQRIEESGAEI
EVGSMPAVMADQIQLMQVFQNLIANGIKFAAGDKSPKIKIWGDRQEDAWVFAVQDN
GIGIDPQFFERIFVIFQRLHTRDEYKGTGMGLAICKKIIIEGHQGGQIWLESNPGEGSTFY
FSIPIGN

cph2 Locus SLL0821 (Manabe K, Nakazawa M. *J Plant Res.* 110: 109-122 (1977))

GB:D64003

SEQ ID NO: 2

MNPNRSLEDFLRNVINKFHRALTLRETQVIVEEARIFLGVDRVKIYKFASDGSGEVL
AEAVNRAALPSLGLHFPVEDIPQAREELGNQRKMIAVDVAHRRKKSHELSGRISP
TEHSNGHYTTVDSCHIQYLLAMGVLSSLTVPVMQDQOLGIMAVHHSKPRRFTEQ
EWETMALLSKEVSLAITQSLSRQVHQQVQEALVQRLETTVAQYGDRPETWQYA
LETVGOAVEADGAVLYIAPDLTGSVAOHYQWNLRFDWGNWLETSLWQELMRGOP

[illegible]

SAAMEPMAAVQSTWEKPRPFTSVAPLPPTNCVPHGYTLGELEQRSDWIAPPESLSAE
 NFQSFLIVPLAADQQWVGSLLRKEKSLVKHWAGKRGIDRRNILPRLSFEAWREETQ
 KLVPTWNRSERKLAQVASTQLYMAITQQFVTRLITQQTAYDPLTQLPNWIIFNRLT
 LALLDALYEGKMVGVLVIAMDRFKRINESFGHKTGDGLLQEVAADRLNQKLSPLAA
 YSPLLSRWHGDGFTILLTOISDNQEMIPLCERLLSTFQEPFFLQGQPIYLTASMGISTA
 PYDGETAESLLKFAEIALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQALTN
 QEFVLYFQPQVALDTGKLLGVEALVRWQHPRLGQVAPDVFIPLAEELGLINHLGQW
 VLETACATHQHFFRETGRRLRMAVNISARQFQDEKWLNSVLECLKRTGMPPEDELE
 EITESLMMEDIKGTVVLLHRLREEGVQVAIDDFGTGYSSLSILKQLPIHRLKIDKSFN
 DLLNEGADTAIIQYVIDLANGLNLETVAEGIESEAQLQRLQKMGCHLGQGYFLTRPL
 PAEAMMTYLYPEQILDGPTPLPKVALPETETEAGQGNVGDRPLPNSLNRENPWTE
 KLHDYVLLKERLQQRNVKEKLVLKIANKIRASLNINDILYSTVTEVRQFLNTDRVVL
FKFNSQWSGQVVTESHNDFCRSIINDEIDDPCFKGHYLRLYREGRVRAVSDIEKADL
ADCHKELLRHYQVKANLVVPVVFNEENLWGLLIAHECKTPRYWQEEDLQLLMELAT
QVAIAIHQGELYEQLETANIRLQQISSLDALTQVGNRYLFDSTLEREWQRLQRIREPL
 ALLLCDVDFFKGFNDNYGHPAGDRCLKKIADAMAKVAKRPTDLVARYGGEEFAILL
 SETSLEGAINVTEALQVEVANLAIPHTVSGTGHVTLSIGIAVYTPERHINPNALVKAA
 DLALYEAKAKGRNQWLAYEGSQLPHVDGEV

Cph3. Locus SLL1473 (RcaE Homolog) a 297 aa histidine kinase homolog

SEQ ID NO: 3

MGKFLPIEFVFLAIAMTCYLWHRQNQERRRIEISIKQQTQRRERFINQITQHIRQSLNLE
TVLNTTVAEVKTLQVDRVLIYRIWQDGTGSAITESVNANYP SILGRFTSDEVFPVEY
HQAYTKGKVRAINIDIDQDDIEICLADFVKQFGVKSCLVVPILQHNRASSLDNESEFP
YLWGLLITHQCAFTRPWQPWEVELMKQLANQVAIAIQQSELYEQLQQLNKDLENR
 VEKRTQQLAATNQSLRMEISERQKTEAALRHTNHTLQSLIAASPRGIFTNLADQIQI
 WNPTAERIFGWTETETIIAHPPELLTSNILLEDYQQFKQKVLSGMVSPSLELKCQKKDGS
 WIEIVLSAAPLLDSEENIAGLVAVVADITEQKRQAEQIRLLQS VVVNTND AVVITEAE
 PIDDPGPRILYVNEAFTKITGYTAEEMLGKTPRVLQGPKTSRTELDRVRQAISQWQS
 VTVEAEVLNDSYKEKKSPLK

cph4 Locus SLL1124 (DivJ homolog; PAS domain) A 1372 aa protein
that is more similar to rcaE than to cph1[Wilde *et al.*. FEBS Lett 406: 89-92 (1997).

GB:U67397 (D90905 or SLL1124)

SEQ ID NO: 4

MTFAATPREVTASAIQWACLCLPGELSAAEALNRWHRHGQRSWEPP
AEAKAFPPWALVLDNDGQLLGLLPDWQLAAALWTEHFSPAIALAELCLPCSLRLDL
EKLPSLGEVMQIFATWGYGWDVIPVADRQHQTWGLLSIGNLIRSVNLCQLWQNLPL
QVTASPPLCLGTETTLGELVHHCFERQISSFPVVYSSPLLPAAPRIPLGNVSLSNYFK
GPNYGSGLDNPIGPDLSPTFPLCTINQTYCHARELLRRQNDDYVIITNISGAFVGWV
GPQQWLATVQPDVLEALQREVEMPRIVQHLEARIVWQQQQQQRNQHLIQKLLSR
NPNLIYLYDLVKNEIVYLNIPGSLDEGGSGGAPIPNPMVETDPRQDLLLPPRYFGLEE
LAALQAHEKKEFNFEFTDGGQSVHYFVVEISAFEIDGSGQTSKILCLAQDVSHGKRA
EAALHTKEQQLQTLVNTIADGIVILDNHDKVYIANPMACQMFGLSKEEFLQSQLGLS
NRGQTEIGINVSPEEEGIGEIKAVPIHWQGEDCRLVTVRDVTDQRVRLKKLRDSEQIH
RSLLEALPNLVWRLSSAGDVWECNQRTLAYFGRRGRKILGNTWQQFIEPGERENVQ
RQWRQGIAAQEFFQLECLWRSDGQYRWHLQVLPLEDRFGSINGWLASSTDIDDL
KEAEKALRNQAQKEKLLSSISQRIRESLKLETILRTTVTEVRRTIHADRVLIHHIQEDG
LGTIAESVVNGQPSVMQMDLSPESFPPECYQRYLNGYIYASRDQLPDCAINCAVQC
FTVAESQSRIVAPIVFDHSLWGLLIVHQCSSSRWTAEIQLMQSLGNQLAIAIQSSL
LYERLQEELSERQRAEQKLLLEVNLQKGIFDVANYMIISTDRRGIISTFNRTAEEILGY
TAAELIGQQTPLIFHDQEEMASEAVQLSQQLQQTIRPNSIDMFAIPAIQWGVYEREWT
YITKTGDRLPVYVSITALRDDQGKVDGLVGVITDLRRQKQIERERQNLDFVVKNSTE
LIVITDLEQKVTFNLQAGQSLIGLENPETAQTTYLSEHISPEYLNFWQMEIIPQVFRSG
AWEGEFSLQHYQTAVEIPVTASVFLQGVNGQH PANLVAIVHDITHIKNAEKRIILAA
LEAEKELGELRSRIFISTTSHEFRTPLAIISSSTGILKKYWPKLDGQRRGQHLEIEESVH
HMVELLDDVL TINRAETKYLPFEPQPLDLVSFCRGITDELQSSTEYHGLLFSYDGLGP
GEIVAFDPKLLRQILTNLLGNAIKYSPSGQPVEFHLQRRGDVGIFSVQDHGIGIGPEDI
PNLFD SFYRG T NVGSIPGTGLGLPIVKKCAELHGGMITVTSQLGQGSRF EVELPLWY
S

**cph5 Locus SLL0041 (locus 1001300) An 891 aa protein, methyl-accepting
chemotaxis protein I. Homology to tsr in last 250 amino acid residues. GB:D64006 Bilin
Binding domain residues 386-550**

SEQ ID NO: 5

MAEAFIAENTAVEDVSPNPNPAIDTDALAALTQSAVELTPPPPINLPKV
ELPPMQPLAPLMAIADPDNLSPMSTSIQAPTQSGGLSLRNKAVLIALLIGLIPAGVIGG
LNLSSVDRLPVPQTEQQVKDSTTKQIRDQILIGLLVTAVGAAFVAYWMVGENTKAQ
TALALKAKHSHRNLDQPLAVAGDELAIDQTIDALSAQVEKLRHQDLSLKQAELL
TELSRANLSDIDEIQGVIQKNLDQARALFGCERLVFYYHPRYQPEAMVVQALDLTTQ
GLIDSKDHPWPWGQEDMPSQIVAINDTSGASISNPHRQWLEQHQVKASLTVPLHRDN
YPLGLLMAHHCQRPHQWEMRERQFLQQLTEELQTTLDLANLIQERNESAQQAQILK
ELTLKISAAINSEQVFDIAAQEIRLALKADRVIVYRFDATWAGTVIVESVAEGYPKAL
GATIADPCFADSYVEKYRSGRIQATRDIYNAGLTPCHIGQLKPFVKANLVAPINYK
GNLLGLLIAHQCSGPRDWHQNEIDLFGQLTVQVGLALERSDLLAQQKIAEVEQRQM
REKMQKRALELLMEVDPVSRGDLTIRAHVTEDEIGTIADSYNATIESLRRIVTQVQT
AASQFTETTTDNEVAVRQLAQQANRQALDVAEALERLQAMNKSIQAVAENAAQAE
SAVQRATQTVDQGEDAMNRTVDGIVAIRETVAATAKQVKRLGESSQKISKVVNLIG
SFADQTNLLALNAAIEAAHAGEEGRGFVVADEVRSLARQSAEATAEIAQLVATIQ
AETNEVVNAMEAGTEQVVVGTKLVEETRRSLNQITAVSAQISGLVEAITSAAIEQSQ
TSESVTQTMALVAQIADKNSSEASGVSATFKELLAVAQSLQEAVKQFKVQ

**cph6 locus SLR1212 (ETR1 homolog; PAS domain) An 844 aa protein,
chromophore domain 461-628**

SEQ ID NO: 6

MAITAFTLGDFQANSYIPHGHCYLWOTPLVWLHVSADFFTAIAYYSI
PLTLLYFLRKRQDIPFPNIIFLSTFILCCGTSHFFDIITLWYPIYWISGTVKASMAIVSII
TVFELIQIVPNALNLKSPTTELATLNLALNQEIKERQTAEIALQELNNNLEKRVEDRTT
QLAKINQQLEQEIEDKTRAKEDLEKNKDQLAQLAAIVESSQDAIISKTLTGDNITSWNE
SAERLFGYTAEEMIGSHITKLIPEELILEEDLIAECIRQQQRINTYETQRQRKDGTKIDV
ALTISPIRDEHKNVVGASKIVRDITARLDVENALRESQYPIEKLANYSPQILYILDPIA
WKNIYVNYQSFEILGYTPEEFKNGGTELLLNIVHPDDIPTLYENKNFWQKSQEGQVL

TTEYRMHRKNGSWRWLRSREVVFARDDYGQVTKVLGTAQDISDSKEQEQRLEYEQ
GRRESLLREITQRIRQSLDLPTIFNTVVQEIRQFLEADRVVIFQFSPDSDFS VGNIVAES
VLAPFKPIINSAIEETCFSNNYAQRYQQGRIQVIEDIHQSHLRQCHIDFLARLQVRANL
VLPLINDAILWGLLCIHQCDSSRVWEQTEIDLLKQITNQFEIAIQQATLYEQAQQELA
SKNQLFVQLTNELEQKKVLLKEIHRVKNNLQIMSSLLYLQFSKASPAIQQLSEEQ
NRIQSMALIHEQLYRSEDLANIDFSQYLKNLTHNICQSYGCNTDSIKIKLLVEQVKVP
LEQSIPLGLIIQELVSNALKHAFPTTEGEISIKFTSMNSHYSLQVWDNGVGISRDIDLE
NTDSLGMQLIYSLTEQLQGELHYEYVGGAQFGLEFSL

cph7 (locus SLR1393, a 950 aa protein chromophore domain 402-620.

Contains a histidine kinase transmitter domain.

SEQ ID NO: 7

MSPSSHGTAVQQAIADQDLEMILQSQDLHNAYRLVVEGLQRGLGVD
RVLLVQNAVFPNRQSRLVAQAIAPARDIMLLDEPCADCRWLHLLGQLPHYGLWTV
WEGEGEFVQLDPVQGEFCRTLGIKSLLHDLPLVINQRHWGVLSLQYLHQARPWPLED
QQFAQRIAHFLCLGLMKTELWIHCQNHKNALQTVVAEGQVQRETYLKSQRERAI
ADVIDKIRFALDLRSLFQTTVTEVRKLLVADRVMIKVRQNKNFSWGEIQAEAQTD
KLCLLPKERVPLSSRWIDHFAKGLILAMDDTDDQRADFDQSMLALAKANLVVPLF
SGDRLWGVLSVHQCDGPRVWESSDIEFALKIALNLGVALQQAELLTESQRRSTALQ
SALGEVEAQKDYLAIAEEERALTRVIEGIROTLELQNI FRATSDEVRHLLSCDRVLV
YRFNPDWSGEFIHESVAQMWEPLKDLQNNFPLWQDTYLQENEGGRYRNHESLAVG
DVETAGFTDCHLDNLRFEIRAF LTPVFVGEQLWGLLGAYQNGAPRHWQAREIHL
LHQIANQLGVAVYQAQLLARFQEQSKTMENTLADLTAIVDNLADGLLVIDLFGRITR
YNPALLAMFDLEGLELLGAGVDAYFPETLNQLLAKPEREEQKLVTADVLSQGRQG
QALITSITSHENGCEYPQCLGAVIMIRDV THEREVERMKTDFLATVSHELRTPLTSIL
GFATVIQDKLNRVIPLEDLAQPHLGKATERVMRNLAIIESEAQRLTVLINDVLDIAK
MEAGQESWQEPCAI GPIIERAIAITIPQAQKKNISLQGDLEPGLPDFIGDENRILQVV
LNLLSNAVKFTP KGLITARSHFHQNYLWVEIIDHGPGIHPADQEKIFEPFQGGGDVL
TDKPQGTGLGLPICKKIVEHHGGTIGVNSSLGRGSTFYFSLPVPVPAVETSPAV

**Cph8 locus SLR1969, a 750 aa protein. CHROMOPHORE DOMAIN
(156-347). Contains a histidine kinase transmitter domain. Adenylate cyclase homology**

SEQ ID NO: 8

MLPAFSPIFRLLPAVTFERLLRFWRTLAQQTGDGVQCFVGDLPSSLK
PPGPSVLEAEVDHRFALLVSPGQWALLEGEQISPHHYAVSITFAQGIIEDFIQKQNL
VVAEAMPHRPETPSGPTIAEQLTLGLLEILNSDSTSFSPEPSLQDSLQASQVKLLSQVI
AQIRQSLDLSEILNNAVTAVQKFLFVDRLVIYQFHYSQPSLTPLEENQIPAPRPRQQY
GEVTYEARRSPEIDTMLGIMTENDCFSQVFSYEQKYLKGAVVAVSDIENHYSSSYCL
VGLLQRYQVRAKLVAPIIVEGQLWGLLIAHQCHHPRQWLDSEKNFLGQIGEHLAVA
IVQSLLYSEVQKQKNNFEKRVIERTKELRDTLMAAQAANLLKSQFINNISHELRTPLT
SIIGLSATLLRWFDHPASLPPAKQQYYLLNIQENGKKLLDQINSIIQLSQLESGQTALN
CQSFSLHTLAQTVIHSLLGVAIKQQINLELDYQINVGQDQFCADQERLDQILTQLLNN
ALKFTPAGTVILRIWKESNQAFQVEDTGIGINEQQLPVLFEAFKVAGDSYTSFYET
GGVGLALTKQLVELHGGYIEVESSPGQGTFITTVIPOQNFPTTKGQVQDKLDAAMP
FNSSVIVIEQDEEIATLICELLTVANYQVIWLIDTTNALQQVELLQPGLIIVDGDVFDV
TEVTRGIKKSRISKVTVFLLSESLSSAEWQALSQKGIDDYLLKPLQPELLLQRVQSIQ
QEPLR

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